



OIEP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/035,343

DATE: 01/17/2002

TIME: 15:50:46

Input Set : A:\2318-290-II.ST25.txt

Output Set: N:\CRF3\01172002\J035343.raw

ENTERED

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3 <110> APPLICANT: Myriad Genetics, Inc.
4   Cimbora, Daniel M.
5   Heichman, Karen
6   Bartel, Paul L.
8 <120> TITLE OF INVENTION: Protein-Protein Interactions
10 <130> FILE REFERENCE: 2318-290-II
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/035,343
C--> 12 <141> CURRENT FILING DATE: 2002-01-04
12 <150> PRIOR APPLICATION NUMBER: US 60/259,572
13 <151> PRIOR FILING DATE: 2001-01-04
15 <160> NUMBER OF SEQ ID NOS: 4
17 <170> SOFTWARE: PatentIn version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 40
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24 <220> FEATURE:
25 <223> OTHER INFORMATION: oligonucleotide primer
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44 <211> LENGTH: 1633
45 <212> TYPE: DNA
46 <213> ORGANISM: Homo sapiens
48 <220> FEATURE:
49 <221> NAME/KEY: CDS
50 <222> LOCATION: (152)..(1633)
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55 actgctgagc agacagccac cgagggccga aattctgagc ctctctctgg acccaggcag      120
57 gagacataca gacaagaag gcaaaactcac c atg gcc tcc acc aat gca gag      172
58                                     Met Ala Ser Thr Asn Ala Glu
59                                     1                               5
61 agc cag ctg cag aga atc atc cga gac ttg caa gat gct gtg aca gaa      220
62 Ser Gln Leu Gln Arg Ile Ile Arg Asp Leu Gln Asp Ala Val Thr Glu

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63	10	15	20	268
65	cta agc aaa gaa ttt	cag gaa gca ggg gaa ccc atc acg gat gac agc		
66	Leu Ser Lys Glu Phe	Gln Glu Ala Gly Glu Pro Ile Thr Asp Asp Ser		
67	25	30	35	316
69	acc agc ttg cat aaa	ttt tct tat aaa ctt gag tat ctc ctg caa ttt		
70	Thr Ser Leu His Lys	Phe Ser Tyr Lys Leu Glu Tyr Leu Leu Gln Phe		
71	40	45	50	364
73	gat cag aaa gag aag	gcc acc ctc ctg gcc aac aag aag gac tac tgg		
74	Asp Gln Lys Glu Lys	Ala Thr Leu Leu Gly Asn Lys Lys Asp Tyr Trp		
75	60	65	70	412
77	gat tac ttc tgt gcc	tgc ctg gcc aag gtg aaa gga gcc aat gat ggg		
78	Asp Tyr Phe Cys Ala	Cys Leu Ala Lys Val Lys Gly Ala Asn Asp Gly		
79	75	80	85	460
81	atc cgc ttt gtc aag	tct atc tca gag ctc cga aca tcc ttg ggg aaa		
82	Ile Arg Phe Val Lys	Ser Ile Ser Glu Leu Arg Thr Ser Leu Gly Lys		
83	90	95	100	508
85	gga aga gca ttt att	cgc tac tcc ttg gtg cac cag agg ttg gca gac		
86	Gly Arg Ala Phe Ile	Arg Tyr Ser Leu Val His Gln Arg Leu Ala Asp		
87	105	110	115	556
89	acc tta cag cag tgc	tto atg aac acc aaa gtg acc agt gac tgg tac		
90	Thr Leu Gln Gln Cys	Phe Met Asn Thr Lys Val Thr Ser Asp Trp Tyr		
91	120	125	130	604
93	tat gca aga agc ccc	ttt ctg cag cca aag ctg agc tcg gac att gtg		
94	Tyr Ala Arg Ser Pro	Phe Leu Gln Pro Lys Leu Ser Ser Asp Ile Val		
95	140	145	150	652
97	ggc caa ctc tat gag	ctg act gag gtt cag ttt gac ctg gcg tcg agg		
98	Gly Gln Leu Tyr Glu	Leu Thr Glu Val Gln Phe Asp Leu Ala Ser Arg		
99	155	160	165	700
101	ggc ttt gac ttg gat	gct gcc tgg cca aca ttt gcc agg agg acg ctg		
102	Gly Phe Asp Leu Asp	Ala Ala Trp Pro Thr Phe Ala Arg Thr Leu		
103	170	175	180	748
105	acc act ggc tct tct	gct tac ctg tgg aaa ccc cct agc cgc agc tcc		
106	Thr Thr Gly Ser Ser	Ala Tyr Leu Trp Lys Pro Pro Ser Arg Ser Ser		
107	185	190	195	796
109	agc atg agc agc ttg	gtg agc agc tac ctg cag act caa gag atg gtg		
110	Ser Met Ser Ser Ser	Leu Val Ser Ser Tyr Leu Gln Thr Gln Glu Met Val		
111	200	205	210	844
113	tcc aac ttt gac ctg	aac agc ccc cta aac aac gag gca ttg gag ggc		
114	Ser Asn Phe Asp Leu	Asn Ser Pro Leu Asn Asn Glu Ala Leu Glu Gly		
115	220	225	230	892
117	ttt gat gag atg cga	cta gag ctg gac cag ttg gag gtg cgg gag aag		
118	Phe Asp Glu Met Arg	Leu Glu Leu Asp Gln Leu Glu Val Arg Glu Lys		
119	235	240	245	940
121	cag cta cgg gag cgc	atg cag cag ctg gac aga gag aac cag gag ctg		
122	Gln Leu Arg Glu Arg	Met Gln Gln Leu Asp Arg Glu Asn Gln Glu Leu		
123	250	255	260	988
125	agg gca gct gtc agc	cag caa ggg gag caa ctg cag aca gag agg gag		
126	Arg Ala Ala Val Ser	Gln Gln Gly Glu Gln Leu Gln Thr Glu Arg Glu		
127	265	270	275	

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129 agg ggg cgc act gca gcg gag gac aac gtt cgc ctc act tgc ttg gta      1036
130 Arg Gly Arg Thr Ala Ala Glu Asp Asn Val Arg Leu Thr Cys Leu Val      295
131 280      285      290
133 gct gag ctc cag aag cag tgg gag gtc acc cag gcc acc cag aac act      1084
134 Ala Glu Leu Gln Lys Gln Trp Glu Val Thr Gln Ala Thr Gln Asn Thr      310
135      300      305      310
137 gtg aag gag ctg cag aca tgc ctg cag ggc ctg gag cta gga gca gca      1132
138 Val Lys Glu Leu Gln Thr Cys Leu Gln Gly Leu Glu Leu Gly Ala Ala      325
139      315      320      325
141 gag aag gag gag gac tac cac aca gcc ctg cgg cgg ctg gag tcc atg      1180
142 Glu Lys Glu Glu Asp Tyr His Thr Ala Leu Arg Arg Leu Glu Ser Met      340
143      330      335      340
145 ctg cag ccc ttg gca cag gag ctt gag gcc aca cgg gac tca ctg gac      1228
146 Leu Gln Pro Leu Ala Gln Glu Leu Glu Ala Thr Arg Asp Ser Leu Asp      355
147      345      350      355
149 aag aaa aac cag cat tta gcc agc ttc cca ggc tgg cta gcc atg gct      1276
150 Lys Lys Asn Gln His Leu Ala Ser Phe Pro Gly Trp Leu Ala Met Ala      375
151 360      365      370      375
153 cag cag aag gca gat acg gca tca gac aca aag ggc cgg caa gaa cct      1324
154 Gln Gln Lys Ala Asp Thr Ala Ser Asp Thr Lys Gly Arg Gln Glu Pro      390
155      380      385      390
157 att ccc agt gat gcg gcc cag gag atg cag gag cta ggg gag aag ctt      1372
158 Ile Pro Ser Asp Ala Ala Gln Glu Met Gln Glu Leu Gly Glu Lys Leu      405
159      395      400      405
161 caa gcc cta gaa agg gag aga acc aag gtc gag gag gtc aac aga cag      1420
162 Gln Ala Leu Glu Arg Glu Arg Thr Lys Val Glu Glu Val Asn Arg Gln      420
163      410      415      420
165 cag agt gcc caa ctg gaa cag ctg gtc aag gag ctt cag ctg aaa gag      1468
166 Gln Ser Ala Gln Leu Glu Gln Leu Val Lys Glu Leu Gln Leu Lys Glu      435
167      425      430      435
169 gat gcc cgg gcc agc ctg gag cgc ctg gtg aag gag atg gcc cca ctc      1516
170 Asp Ala Arg Ala Ser Leu Glu Arg Leu Val Lys Glu Met Ala Pro Leu      455
171 440      445      450      455
173 cag gag gag ttg tct ggg aag gga cag gag gca gac cag ctc tgg cga      1564
174 Gln Glu Glu Leu Ser Gly Lys Gly Gln Glu Ala Asp Gln Leu Trp Arg      470
175      460      465      470
177 cgg ctg cag gag ttg ctg gcc cac acg agc tcc tgg gag gag gac cta      1612
178 Arg Leu Gln Glu Leu Leu Ala His Thr Ser Ser Trp Glu Glu Glu Leu      485
179      475      480      485
181 gca gag ttg agg cgg gag aaa      1633
182 Ala Glu Leu Arg Arg Glu Lys
183      490
186 <210> SEQ ID NO: 4
187 <211> LENGTH: 494
188 <212> TYPE: PRT
189 <213> ORGANISM: Homo sapiens
191 <400> SEQUENCE: 4
193 Met Ala Ser Thr Asn Ala Glu Ser Gln Leu Gln Arg Ile Ile Arg Asp      15
194 1      5      10

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197 Leu Gln Asp Ala Val Thr Glu Leu Ser Lys Glu Phe Gln Glu Ala Gly
198      20      25      30
201 Glu Pro Ile Thr Asp Asp Ser Thr Ser Leu His Lys Phe Ser Tyr Lys
202      35      40      45
205 Leu Glu Tyr Leu Leu Gln Phe Asp Gln Lys Glu Lys Ala Thr Leu Leu
206      50      55      60
209 Gly Asn Lys Lys Asp Tyr Trp Asp Tyr Phe Cys Ala Cys Leu Ala Lys
210      65      70      75      80
213 Val Lys Gly Ala Asn Asp Gly Ile Arg Phe Val Lys Ser Ile Ser Glu
214      85      90      95
217 Leu Arg Thr Ser Leu Gly Lys Gly Arg Ala Phe Ile Arg Tyr Ser Leu
218      100      105      110
221 Val His Gln Arg Leu Ala Asp Thr Leu Gln Gln Cys Phe Met Asn Thr
222      115      120      125
225 Lys Val Thr Ser Asp Trp Tyr Tyr Ala Arg Ser Pro Phe Leu Gln Pro
226      130      135      140
229 Lys Leu Ser Ser Asp Ile Val Gly Gln Leu Tyr Glu Leu Thr Glu Val
230      145      150      155      160
233 Gln Phe Asp Leu Ala Ser Arg Gly Phe Asp Leu Asp Ala Ala Trp Pro
234      165      170      175
237 Thr Phe Ala Arg Arg Thr Leu Thr Thr Gly Ser Ser Ala Tyr Leu Trp
238      180      185      190
241 Lys Pro Pro Ser Arg Ser Ser Ser Met Ser Ser Leu Val Ser Ser Tyr
242      195      200      205
245 Leu Gln Thr Gln Glu Met Val Ser Asn Phe Asp Leu Asn Ser Pro Leu
246      210      215      220
249 Asn Asn Glu Ala Leu Glu Gly Phe Asp Glu Met Arg Leu Glu Leu Asp
250      225      230      235      240
253 Gln Leu Glu Val Arg Glu Lys Gln Leu Arg Glu Arg Met Gln Gln Leu
254      245      250      255
257 Asp Arg Glu Asn Gln Glu Leu Arg Ala Ala Val Ser Gln Gln Gly Glu
258      260      265      270
261 Gln Leu Gln Thr Glu Arg Glu Arg Gly Arg Thr Ala Ala Glu Asp Asn
262      275      280      285
265 Val Arg Leu Thr Cys Leu Val Ala Glu Leu Gln Lys Gln Trp Glu Val
266      290      295      300
269 Thr Gln Ala Thr Gln Asn Thr Val Lys Glu Leu Gln Thr Cys Leu Gln
270      305      310      315      320
273 Gly Leu Glu Leu Gly Ala Ala Glu Lys Glu Glu Asp Tyr His Thr Ala
274      325      330      335
277 Leu Arg Arg Leu Glu Ser Met Leu Gln Pro Leu Ala Gln Glu Leu Glu
278      340      345      350
281 Ala Thr Arg Asp Ser Leu Asp Lys Lys Asn Gln His Leu Ala Ser Phe
282      355      360      365
285 Pro Gly Trp Leu Ala Met Ala Gln Gln Lys Ala Asp Thr Ala Ser Asp
286      370      375      380
289 Thr Lys Gly Arg Gln Glu Pro Ile Pro Ser Asp Ala Ala Gln Glu Met
290      385      390      395      400
293 Gln Glu Leu Gly Glu Lys Leu Gln Ala Leu Glu Arg Glu Arg Thr Lys

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Input Set : A:\2318-290-11\S1251021
Output Set: N:\CRF3\01172002\J035343.raw

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294																
297	Val	Glu	Glu	Val	Asn	Arg	Gln	Gln	Ser	Ala	Gln	Leu	Glu	Gln	Leu	Val
298				420					425					430		
301	Lys	Gly	Leu	Gln	Leu	Lys	Glu	Asp	Ala	Arg	Ala	Ser	Leu	Glu	Arg	Leu
302			435					440					445			
305	Val	Lys	Glu	Met	Ala	Pro	Leu	Gln	Glu	Glu	Leu	Ser	Gly	Lys	Gly	Gln
306			450				455					460				
309	Glu	Ala	Ala	Asp	Gln	Leu	Trp	Arg	Gln	Leu	Gln	Glu	Leu	Leu	Ala	His
310	465					470					475					480
313	Ser	Ser	Trp	Glu	Glu	Glu	Leu	Ala	Glu	Leu	Arg	Arg	Glu	Lys		
314					485					490						

VERIFICATION SUMMARY

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Output Set: N:\CRF3\01172002\J035343.raw

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:22 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:34 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2